

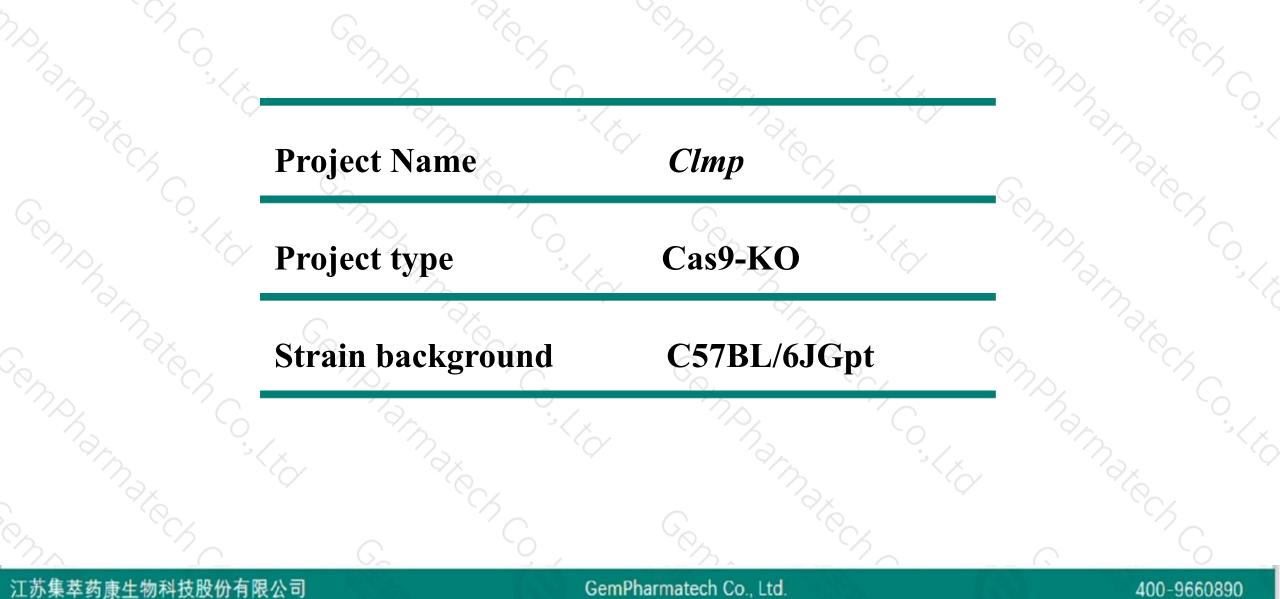
Clmp Cas9-KO Strategy

Designer: Reviewer: Design Date:

Ruirui Zhang Huimin Su 2019-9-20

Project Overview

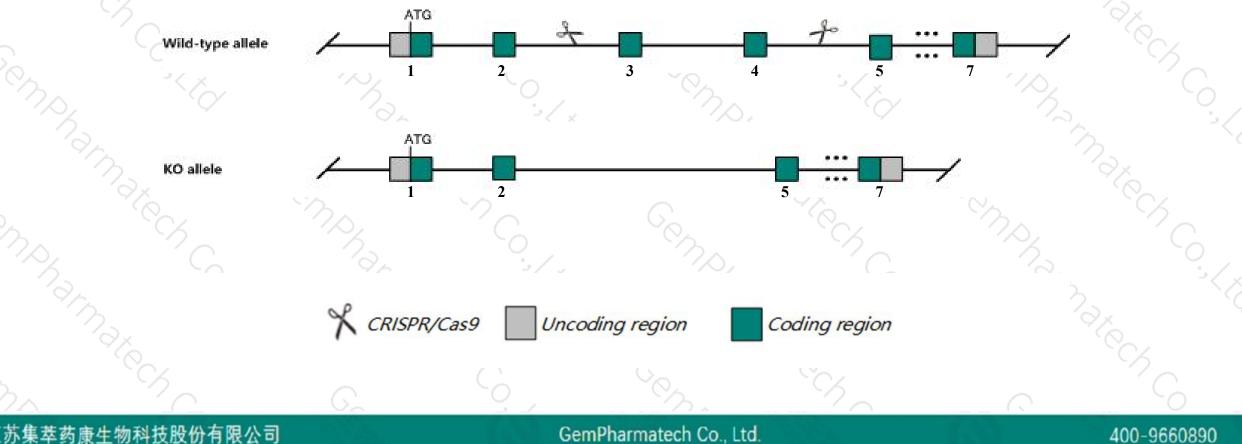




Knockout strategy



This model will use CRISPR/Cas9 technology to edit the *Clmp* gene. The schematic diagram is as follows:



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- The Clmp gene has 4 transcripts. According to the structure of Clmp gene, exon3-exon4 of Clmp-201 (ENSMUST00000034522.7) transcript is recommended as the knockout region. The region contains 370bp coding sequence. Knock out the region will result in disruption of protein function.
- > In this project we use CRISPR/Cas9 technology to modify *Clmp* gene. The brief process is as follows: CRISPR/Cas9 system



- According to the existing MGI data, Mice homozygous for a targeted null allele exhibit reduced viability, bilateral hydronephrosis, increased mean systolic blood pressure, and exhibit several blood chemistry and neurological anomalies. Null mice are samller than controls.
- > The *Clmp* gene is located on the Chr9. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of the gene knockout on gene transcription, RNA splicing and protein translation cannot be predicted at the existing technology level.

Gene information (NCBI)



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400-9660890

CImp CXADR-like membrane protein [Mus musculus (house mouse)]

Gene ID: 71566, updated on 12-Aug-2019

Summary

Official Symbol	CImp provided by MGI
Official Full Name	CXADR-like membrane protein provided by MGI
Primary source	MGI:MGI:1918816
See related	Ensembl:ENSMUSG0000032024
Gene type	protein coding
RefSeq status	VALIDATED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires;
Also known as	Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus ACAM; ASP5; AW557819; 9030425E11Rik
Expression	
Orthologs	human all

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Transcript information (Ensembl)



The gene has 4 transcripts, all transcripts are shown below:

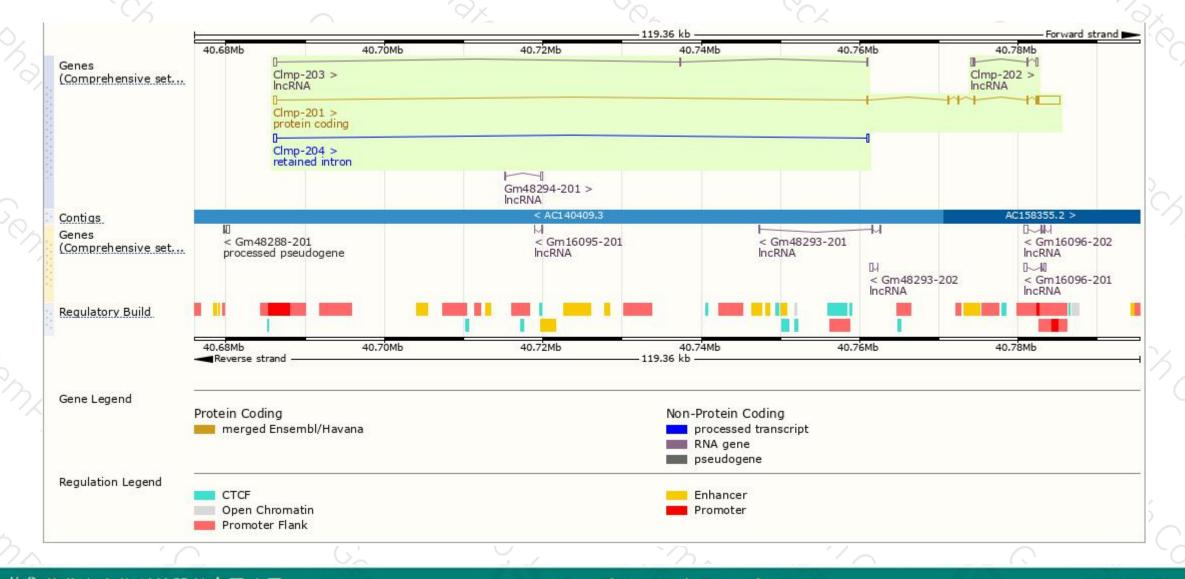
Name 🖕	Transcript ID	bp 🛔	Protein 🖕	Biotype 🍦	CCDS 🖕	UniProt 🖕	Flags		
Clmp-201	ENSMUST0000034522.7	4154	<u>373aa</u>	Protein coding	<u>CCDS23082</u> 교	<u>Q8R373</u> @	TSL:1	GENCODE basic	APPRIS P1
Clmp-204	ENSMUST00000141759.1	608	No protein	Retained intron	3 .		TSL:2		
Clmp-203	ENSMUST00000139577.1	634	No protein	IncRNA	3		TSL:3		
Clmp-202	ENSMUST00000134153.1	616	No protein	IncRNA	3	(a)	TSL:3		

The strategy is based on the design of Clmp-201 transcript, The transcription is shown below



Genomic location distribution





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Protein domain



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ENSMUSP00000034 Transmembrane heli MobiDB lite Low complexity (Seg) Cleavage site (Sign			а н .нт				
Superfamily SMART		lin-like domain supe ulin V-set domain	erfamily				
	Immunoglobu	in subtype 2					
Pfam.	Immunoglobulin Immunoglobulin	and the second se	PF13927				6.
PROSITE profiles PANTHER	Immunoglobi PTHR44783	ulin-like domain		, i			
Gene3D CDD	Immunaglobulin-	like fold	сдоооэ6				2
All sequence SNPs/i	Sequence variants (dbSNP and all oth	er sources)	U		a a	1 34
Variant Legend	synonymous v	ariant			1.1.		
Scale bar	0 40	80	120 160	200	240	280 320	373
20	G.	0	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	A	2		6

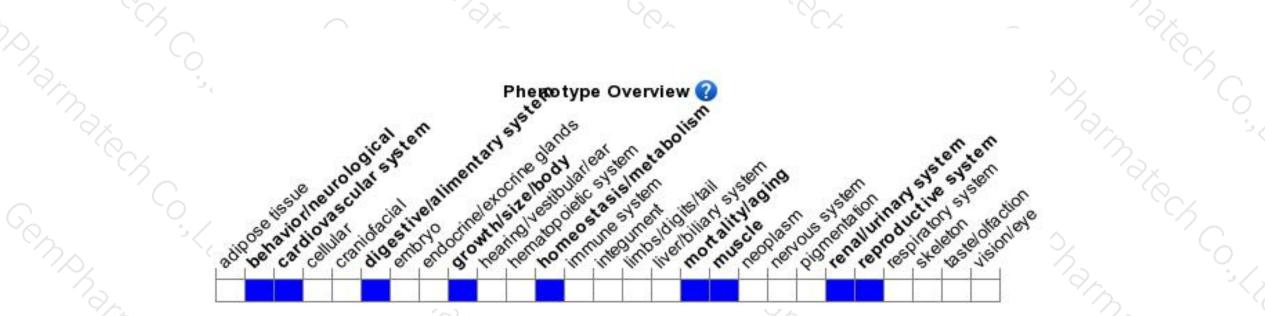
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Mouse phenotype description(MGI)





Phenotypes affected by the gene are marked in blue.Data quoted from MGI database(http://www.informatics.jax.org/).

According to the existing MGI data, Mice homozygous for a targeted null allele exhibit reduced viability, bilateral hydronephrosis, increased mean systolic blood pressure, and exhibit several blood chemistry and neurological anomalies. Null mice are samller than controls.

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If you have any questions, you are welcome to inquire. Tel: 400-9660890



